

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/731,457B

DATE: 01/16/2002

TIME: 13:34:30

Input Set : A:\rts-182.txt

Output Set: N:\CRF3\01162002\I731457B.raw

ENTERED

4 <110> APPLICANT: Ian Popoff
 5 Jacqueline Wyatt
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN
 1, P127
 8 EXPRESSION
 10 <130> FILE REFERENCE: RTS-0182
 12 <140> CURRENT APPLICATION NUMBER: US/09/731,457B
 13 <141> CURRENT FILING DATE: 2000-12-06
 15 <160> NUMBER OF SEQ ID NOS: 87
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 20
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Artificial Sequence
 23 <220> FEATURE:
 25 <223> OTHER INFORMATION: Antisense Oligonucleotide
 27 <400> SEQUENCE: 1
 28 tccgtcctcg ctctcaggg 20
 31 <210> SEQ ID NO: 2
 32 <211> LENGTH: 20
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Artificial Sequence
 36 <220> FEATURE:
 38 <223> OTHER INFORMATION: Antisense Oligonucleotide
 40 <400> SEQUENCE: 2
 41 atgcattctg cccccaagga 20
 44 <210> SEQ ID NO: 3
 45 <211> LENGTH: 4193
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Homo sapiens
 49 <220> FEATURE:
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 52 <221> NAME/KEY: CDS
 53 <222> LOCATION: (101)...(3523)
 55 <400> SEQUENCE: 3
 56 gtggagttcg ctgggctgt tgggggcccac ctgtcttttc gcttctgccc ctctttctag 60
 58 tctcgcgtc gagtcccgac gggcgcctcc aagcctcgac atg tgg tac aac tac 115
 59 Met Ser Tyr Asn Tyr
 60 1 5
 62 gtg gta acg gcc cag aag ccc acc gcc gtg aac ggc tgc gtg acc gga 163
 63 Val Val Thr Ala Gln Lys Pro Thr Ala Val Asn Gly Cys Val Thr Gly
 64 10 15 20
 66 cac ttt act tgg gcc gaa gac tta aac ctg ttg att gcc aaa aac acg 211
 67 His Phe Thr Ser Ala Glu Asp Leu Asn Leu Leu Ile Ala Lys Asn Thr
 68 25 30 35
 70 aga tta gag atc tat ttg gtc acc gcc gag ggg ctt cgg ccc gtc aaa 259
 71 Arg Leu Glu Ile Tyr Val Val Thr Ala Glu Gly Leu Arg Pro Val Lys
 72 40 45 50
 74 gag gtg gcc atg tat ggg aag att ggg gtc atg gag ctt ttc aag ccc 307

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75 Glu Val Gly Met Tyr Gly Lys Ile Ala Val Met Glu Leu Phe Arg Pro
76      55      60      65
78 aag ggg gag agc aag gac ctg ctg ttt atc ttg aca gcg aag tac aat      355
79 Lys Gly Glu Ser Lys Asp Leu Leu Phe Ile Leu Thr Ala Lys Tyr Asn
80 70      75      80      85
82 gcc tgc atc ctg gag tat aaa cag agt ggc gag agc att gac atc att      403
83 Ala Cys Ile Leu Glu Tyr Lys Gln Ser Gly Glu Ser Ile Asp Ile Ile
84      90      95      100
86 acg cga gcc cat ggc aat gtc cag gac cgc att ggc cgc ccc tca gag      451
87 Thr Arg Ala His Gly Asn Val Gln Asp Arg Ile Gly Arg Pro Ser Glu
88      105      110      115
90 acc ggc att att ggc atc att gac cct gag tgc cgg atg att ggc ctg      499
91 Thr Gly Ile Ile Gly Ile Ile Asp Pro Glu Cys Arg Met Ile Gly Leu
92      120      125      130
94 cgt ctc tat gat ggc ctt ttc aag gtt att cca cta gat cgc gat aat      547
95 Arg Leu Tyr Asp Gly Leu Phe Lys Val Ile Pro Leu Asp Arg Asp Asn
96      135      140      145
98 aaa gaa ctc aag gcc ttc aac atc cgc ctg gag gag ctg cat gtc att      595
99 Lys Glu Leu Lys Ala Phe Asn Ile Arg Leu Glu Glu Leu His Val Ile
100 150      155      160      165
102 gat gtc aag ttc cta tat ggt tgc caa gca cct act att tgc ttt gtc      643
103 Asp Val Lys Phe Leu Tyr Gly Cys Gln Ala Pro Thr Ile Cys Phe Val
104      170      175      180
106 tac cag gac cct cag ggg cgg cac gta aaa acc tat gag gtg tct ctc      691
107 Tyr Gln Asp Pro Gln Gly Arg His Val Lys Thr Tyr Glu Val Ser Leu
108      185      190      195
110 cga gaa aag gaa ttc aat aag ggc cct tgg aaa cag gaa aat gtc gaa      739
111 Arg Glu Lys Glu Phe Asn Lys Gly Pro Trp Lys Gln Glu Asn Val Glu
112      200      205      210
114 gct gaa gct tcc atg gtg atc qca gtc cca gag ccc ttt ggg ggg gcc      787
115 Ala Glu Ala Ser Met Val Ile Ala Val Pro Glu Pro Phe Gly Gly Ala
116      215      220      225
118 atc atc att gga cag gag tca atc acc tat cac aat ggt gac aaa tac      835
119 Ile Ile Ile Gly Gln Glu Ser Ile Thr Tyr His Asn Gly Asp Lys Tyr
120 230      235      240      245
122 ctg gct att gcc cct cct atc atc aag caa agc acg att gtg tgc cac      883
123 Leu Ala Ile Ala Pro Pro Ile Ile Lys Gln Ser Thr Ile Val Cys His
124      250      255      260
126 aat cga gtg gac cct aat ggc tca aga tac ctg ctg gga gac atg gaa      931
127 Asn Arg Val Asp Pro Asn Gly Ser Arg Tyr Leu Leu Gly Asp Met Glu
128      265      270      275
130 ggc cgg ctc ttc atg ctg ctt ttg gag aag gag gaa cag atg gat ggc      979
131 Gly Arg Leu Phe Met Leu Leu Leu Glu Lys Glu Glu Gln Met Asp Gly
132      280      285      290
134 acc gtc act ctc aag gat ctc cgt gta gaa ctc ctt gga gag acc tct      1027
135 Thr Val Thr Leu Lys Asp Leu Arg Val Glu Leu Leu Gly Glu Thr Ser
136      295      300      305
138 att gct gag tgc ttg aca tac ctt gat aat ggt gtt gtg ttt gtc ggg      1075
139 Ile Ala Glu Cys Leu Thr Tyr Leu Asp Asn Gly Val Val Phe Val Gly

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140	310		315		320		325	
142	tct cgc ctg ggt gac tcc cag ctt gtg aag ctc aac gtt gac agt aat	1123						
143	Ser Arg Leu Gly Asp Ser Gln Leu Val Lys Leu Asn Val Asp Ser Asn							
144		330		335		340		
146	gaa caa ggc tcc tat gta gtg gcc atg gaa acc ttt acc aac tta gga	1171						
147	Glu Gln Gly Ser Tyr Val Val Ala Met Glu Thr Phe Thr Asn Leu Gly							
148		345		350		355		
150	ccc att gtc gat atg tgc gtg gtg gac ctg gag agg cag ggg cag ggg	1219						
151	Pro Ile Val Asp Met Cys Val Val Asp Leu Glu Arg Gln Gly Gln Gly							
152		360		365		370		
154	cag ctg gtc act tgc tct ggg gct ttc aag gaa ggt tct ttg cgg atc	1267						
155	Gln Leu Val Thr Cys Ser Gly Ala Phe Lys Glu Gly Ser Leu Arg Ile							
156		375		380		385		
158	atc cgg aat gga att gga atc cac gag cat gcc agc att gac tta cca	1315						
159	Ile Arg Asn Gly Ile Gly Ile His Glu His Ala Ser Ile Asp Leu Pro							
160	390		395		400		405	
162	ggc atc aaa gga tta tgg cca ctg cgg tct gac cct aat cgt gag act	1363						
163	Gly Ile Lys Gly Leu Trp Pro Leu Arg Ser Asp Pro Asn Arg Glu Thr							
164		410		415		420		
166	gat gac act ttg gtg ctc tct ttt gtg ggc cag aca aga gtt ctc atg	1411						
167	Asp Asp Thr Leu Val Leu Ser Phe Val Gly Gln Thr Arg Val Leu Met							
168		425		430		435		
170	tta aat gga gag gag gta gaa gaa acc gaa ctg atg ggt ttc gtg gat	1459						
171	Leu Asn Gly Glu Glu Val Glu Glu Thr Glu Leu Met Gly Phe Val Asp							
172		440		445		450		
174	gat cag cag act ttc ttc tgt ggc aac gtg gct cat cag cag ctt atc	1507						
175	Asp Gln Gln Thr Phe Phe Cys Gly Asn Val Ala His Gln Gln Leu Ile							
176		455		460		465		
178	cag atc act tca gca tgg gtg agg ttg gtc tct caa gaa ccc aaa gct	1555						
179	Gln Ile Thr Ser Ala Ser Val Arg Leu Val Ser Gln Glu Pro Lys Ala							
180	470		475		480		485	
182	ctg gtc agt gaa tgg aag gag cct cag gcc aag aac atc agt gtg gcc	1603						
183	Leu Val Ser Glu Trp Lys Glu Pro Gln Ala Lys Asn Ile Ser Val Ala							
184		490		495		500		
186	tcc tgc aat agc agc cag gtg gtg gtg gct gta ggc agg gcc ctc tac	1651						
187	Ser Cys Asn Ser Ser Gln Val Val Val Ala Val Gly Arg Ala Leu Tyr							
188		505		510		515		
190	tat ctg cag atc cat cct cag gag ctc cgg cag atc agc cac aca gag	1699						
191	Tyr Leu Gln Ile His Pro Gln Glu Leu Arg Gln Ile Ser His Thr Glu							
192		520		525		530		
194	atg gaa cat gaa gtg gct tgc ttg gac atc acc cca tta gga gac agc	1747						
195	Met Glu His Glu Val Ala Cys Leu Asp Ile Thr Pro Leu Gly Asp Ser							
196		535		540		545		
198	aat gga ctg tcc cct ctt tgt gcc att ggc ctc tgg acg gac atc tgg	1795						
199	Asn Gly Leu Ser Pro Leu Cys Ala Ile Gly Leu Trp Thr Asp Ile Ser							
200	550		555		560		565	
202	gct cgt atc ttg aag ttg ccc tct ttt gaa cta ctg cac aag gag atg	1843						
203	Ala Arg Ile Leu Lys Leu Pro Ser Phe Glu Leu Leu His Lys Glu Met							
204		570		575		580		

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206	ctg	ggt	gga	gag	atc	att	cct	cgc	tcc	atc	ctg	atg	acc	acc	ttt	gag	1891
207	Leu	Gly	Gly	Glu	Ile	Ile	Pro	Arg	Ser	Ile	Leu	Met	Thr	Thr	Phe	Glu	
208				585					590						595		
210	agt	agc	cat	tac	ctc	ctt	tgt	gcc	ttg	gga	gat	gga	ggg	ctt	ttc	tac	1939
211	Ser	Ser	His	Tyr	Leu	Leu	Cys	Ala	Leu	Gly	Asp	Gly	Ala	Leu	Phe	Tyr	
212			600					605					610				
214	ttt	ggg	ctc	aac	att	gag	aca	ggt	ctg	ttg	agc	gac	cgt	aag	aag	gtg	1987
215	Phe	Gly	Leu	Asn	Ile	Glu	Thr	Gly	Leu	Leu	Ser	Asp	Arg	Lys	Lys	Val	
216		615					620					625					
218	act	ttg	ggc	acc	cag	ccc	acc	gta	ttg	agg	act	ttt	cgt	tct	ctt	tct	2035
219	Thr	Leu	Gly	Thr	Gln	Pro	Thr	Val	Leu	Arg	Thr	Phe	Arg	Ser	Leu	Ser	
220	630					635					640					645	
222	acc	acc	aac	gtc	ttt	gct	tgt	tct	gac	cgc	ccc	act	gtc	atc	tat	agc	2083
223	Thr	Thr	Asn	Val	Phe	Ala	Cys	Ser	Asp	Arg	Pro	Thr	Val	Ile	Tyr	Ser	
224				650					655					660			
226	agc	aac	cac	aaa	ttg	gtc	ttc	tea	aat	gtc	aac	ctc	aag	gaa	gtg	aac	2131
227	Ser	Asn	His	Lys	Leu	Val	Phe	Ser	Asn	Val	Asn	Leu	Lys	Glu	Val	Asn	
228			665					670					675				
230	tac	atg	tgt	ccc	ctc	aat	tea	gat	ggc	tat	cct	gac	agc	ctg	ggg	ctg	2179
231	Tyr	Met	Cys	Pro	Leu	Asn	Ser	Asp	Gly	Tyr	Pro	Asp	Ser	Leu	Ala	Leu	
232		680					685					690					
234	gcc	aac	aat	agc	acc	ctc	acc	att	ggc	acc	atc	gat	gag	atc	cag	aag	2227
235	Ala	Asn	Asn	Ser	Thr	Leu	Thr	Ile	Gly	Thr	Ile	Asp	Glu	Ile	Gln	Lys	
236		695				700					705						
238	ctg	cac	att	cgc	aca	gtt	ccc	ctc	tat	gag	tct	cca	agg	aag	atc	tgc	2275
239	Leu	His	Ile	Arg	Thr	Val	Pro	Leu	Tyr	Glu	Ser	Pro	Arg	Lys	Ile	Cys	
240	710					715					720					725	
242	tac	cag	gaa	gtg	tcc	cag	tgt	ttc	ggg	gtc	ctc	tcc	agc	cgc	att	gaa	2323
243	Tyr	Gln	Glu	Val	Ser	Gln	Cys	Phe	Gly	Val	Leu	Ser	Ser	Arg	Ile	Glu	
244			730					735					740				
246	gtc	caa	gac	acg	agt	ggg	ggc	acg	aca	gcc	ttg	agg	ccc	agc	gct	agc	2371
247	Val	Gln	Asp	Thr	Ser	Gly	Gly	Thr	Ala	Leu	Arg	Pro	Ser	Ala	Ser		
248			745					750					755				
250	acc	cag	gct	ctg	tcc	agc	agt	gta	agc	tcc	agc	aag	ctg	ttc	tcc	agc	2419
251	Thr	Gln	Ala	Leu	Ser	Ser	Ser	Val	Ser	Ser	Ser	Lys	Leu	Phe	Ser	Ser	
252			760					765					770				
254	agc	act	gct	cct	cat	gag	acc	tcc	ttt	gga	gaa	gag	gtg	gag	gtg	cac	2467
255	Ser	Thr	Ala	Pro	His	Glu	Thr	Ser	Phe	Gly	Glu	Glu	Val	Glu	Val	His	
256		775				780					785						
258	aac	cta	ctt	atc	att	gac	caa	cac	acc	ttt	gaa	gtg	ctt	cat	gcc	cac	2515
259	Asn	Leu	Leu	Ile	Ile	Asp	Gln	His	Thr	Phe	Glu	Val	Leu	His	Ala	His	
260	790					795					800					805	
262	cag	ttt	ctg	cag	aat	gaa	tat	gcc	ctc	agt	ctg	gtt	tcc	tgc	aag	ctg	2563
263	Gln	Phe	Leu	Gln	Asn	Glu	Tyr	Ala	Leu	Ser	Leu	Val	Ser	Cys	Lys	Leu	
264			810							815					820		
266	ggc	aaa	gac	ccc	aac	act	tac	ttc	att	gtg	ggc	aca	gca	atg	gtg	tat	2611
267	Gly	Lys	Asp	Pro	Asn	Thr	Tyr	Phe	Ile	Val	Gly	Thr	Ala	Met	Val	Tyr	
268			825						830				835				
270	cct	gaa	gaq	gca	gag	ccc	aag	caq	ggt	cgc	att	gtg	gtc	ttt	cag	tat	2659

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271	Pro	Glu	Glu	Ala	Glu	Pro	Lys	Gln	Gly	Arg	Ile	Val	Val	Phe	Gln	Tyr	
272			840					845					850				
274	tgc	gat	gga	aaa	cta	cag	act	gtg	gct	gaa	aag	gaa	gtg	aaa	ggg	gcc	2707
275	Ser	Asp	Gly	Lys	Leu	Gln	Ihr	Val	Ala	Glu	Lys	Gln	Val	Lys	Gly	Ala	
276			855					860					865				
278	gtg	tac	tct	atg	gtg	gaa	ttt	aac	ggg	aag	ctg	tta	gcc	agc	atc	aat	2755
279	Val	Tyr	Ser	Met	Val	Glu	Phe	Asn	Gly	Lys	Leu	Leu	Ala	Ser	Ile	Asn	
280	870						875					880				885	
282	agc	acg	gtg	cgg	ctc	tat	gag	tgg	aca	aca	gag	aag	gag	ctg	cgc	act	2803
283	Ser	Ihr	Val	Arg	Leu	Tyr	Glu	Trp	Thr	Thr	Glu	Lys	Gln	Leu	Arg	Thr	
284						890					895				900		
286	gag	tgc	aac	cac	tac	aac	aac	atc	atg	gcc	ctc	tac	ctg	aag	acc	aag	2851
287	Glu	Cys	Asn	His	Tyr	Asn	Asn	Ile	Met	Ala	Leu	Tyr	Leu	Lys	Thr	Lys	
288				905						910				915			
290	ggc	gac	ttc	atc	ctg	gtg	ggc	gac	ctt	atg	cgc	tca	gtg	ctg	ctg	ctt	2899
291	Gly	Asp	Phe	Ile	Leu	Val	Gly	Asp	Leu	Met	Arg	Ser	Val	Leu	Leu	Leu	
292			920					925					930				
294	gcc	tac	aag	ccc	atg	gaa	gga	aac	ttt	gaa	gag	att	gct	cga	gac	ttt	2947
295	Ala	Tyr	Lys	Pro	Met	Glu	Gly	Asn	Phe	Glu	Glu	Ile	Ala	Arg	Asp	Phe	
296			935					940					945				
298	aat	ccc	aac	tgg	atg	agt	gct	gtg	gaa	atc	ttg	gat	gat	gac	aat	ttt	2995
299	Asn	Pro	Asn	Trp	Met	Ser	Ala	Val	Glu	Ile	Leu	Asp	Asp	Asp	Asn	Phe	
300	950					955					960				965		
302	ctg	ggg	gct	gaa	aat	gcc	ttt	aac	ttg	ttt	gtg	tgt	caa	aag	gat	agc	3043
303	Leu	Gly	Ala	Glu	Asn	Ala	Phe	Asn	Leu	Phe	Val	Cys	Gln	Lys	Asp	Ser	
304					970					975				980			
306	gct	gcc	acc	act	gac	gag	gag	cgg	cag	cac	ctc	cag	gag	gtt	ggt	ctt	3091
307	Ala	Ala	Thr	Thr	Asp	Glu	Glu	Arg	Gln	His	Leu	Gln	Glu	Val	Gly	Leu	
308				985				990					995				
310	ttc	cac	ctg	ggc	gag	ttt	gtc	aat	gtc	ttt	tgc	cac	ggc	tct	ctg	gta	3139
311	Phe	His	Leu	Gly	Glu	Phe	Val	Asn	Val	Phe	Cys	His	Gly	Ser	Leu	Val	
312			1000					1005					1010				
314	atg	cag	aat	ctg	ggt	gag	act	tcc	acc	ccc	aca	caa	ggc	tgc	gtg	ctc	3187
315	Met	Gln	Asn	Leu	Gly	Glu	Thr	Ser	Thr	Pro	Thr	Gln	Gly	Ser	Val	Leu	
316			1015				1020					1025					
318	ttc	ggc	acg	gtc	aac	ggc	atg	ata	ggg	ctg	gtg	acc	tca	ctg	tca	gag	3235
319	Phe	Gly	Thr	Val	Asn	Gly	Met	Ile	Gly	Leu	Val	Thr	Ser	Leu	Ser	Glu	
320	1030					1035				1040				1045			
322	agc	tgg	tac	aac	ctc	ctg	ctg	gac	atg	cag	aat	cga	ctc	aat	aaa	gtc	3283
323	Ser	Trp	Tyr	Asn	Leu	Leu	Leu	Asp	Met	Gln	Asn	Arg	Leu	Asn	Lys	Val	
324				1050						1055				1060			
326	atc	aaa	agt	gtg	ggg	aag	atc	gag	cac	tcc	ttc	tgg	aga	tcc	ttt	cac	3331
327	Ile	Lys	Ser	Val	Gly	Lys	Ile	Glu	His	Ser	Phe	Trp	Arg	Ser	Phe	His	
328				1065					1070					1075			
330	acc	gag	cgg	aag	aca	gaa	cca	gcc	aca	ggt	ttc	atc	gac	ggt	gac	ttg	3379
331	Thr	Glu	Arg	Lys	Thr	Glu	Pro	Ala	Thr	Gly	Phe	Ile	Asp	Gly	Asp	Leu	
332			1080					1085					1090				
334	att	gag	agt	ttc	ctg	gat	att	agc	cgc	ccc	aag	atg	cag	gag	gtg	gtg	3427
335	Ile	Glu	Ser	Phe	Leu	Asp	Ile	Ser	Arg	Pro	Lys	Met	Gln	Glu	Val	Val	

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